

Claims

What is claimed is:

5. 1. A nucleic acid probe comprising a nucleic acid sequence 7 to 500 nucleotide bases in length that specifically binds under selective binding conditions to a nucleic acid sequence comprising at least one variance in a gene selected from the group consisting of Human glutamate dehydrogenase (EC 1.4.1.3., GDH), Cytochrome P-450 (CYP3A4), Human acyl coenzyme A:cholesterol acyltransferase, Homo sapiens P-type ATPase FIC1, Human neutral amino acid transporter B, Human E16, H.sapiens canalicular multidrug resistance protein, Human organic anion transporting polypeptide (OATP), Carboxylesterase I, H.sapiens REC1L or a sequence complementary thereto or an RNA equivalent.
10. 2. The probe of claim 1, wherein said probe comprises a nucleic acid sequence 200 nucleotide bases or fewer in length.
15. 3. The probe of claim 1, wherein said nucleic acid sequence is 100 or fewer nucleotide bases in length.
20. 4. The probe of claim 1, wherein said nucleic acid sequence is 25 or fewer nucleotide bases in length.
25. 5. The probe of claim 1, wherein said probe comprises DNA.
30. 6. The probe of claim 1, wherein said probe comprises DNA and at least one nucleic acid analog.
35. 7. The probe of claim 1, wherein said probe comprises peptide nucleic acid (PNA).
8. The probe of claim 1, further comprising a detectable label.
9. The probe of claim 8, wherein said detectable label is a fluorescent label.
40. 10. The probe of claim 1, wherein said at least one variance is listed in Table 3.
11. An isolated, purified or enriched nucleic acid sequence of 15 to 500 nucleotides in length, comprising at least one variance, wherein said sequence has the base sequence of a portion of an allele of a gene selected from the group consisting of Human glutamate dehydrogenase (EC 1.4.1.3., GDH), Cytochrome P-

0 5 5 4 3 2 1 0 8 2 5 0

450 (CYP3A4), Human acyl coenzyme A:cholesterol acyltransferase, Homo sapiens P-type ATPase FIC1, Human neutral amino acid transporter B, Human E16, H.sapiens canalicular multidrug resistance protein, Human organic anion transporting polypeptide (OATP), Carboxylesterase I, H.sapiens REC1L or a sequence complementary thereto or an RNA equivalent.

12. The nucleic acid sequence of claim 11, wherein said nucleic acid sequence is 15 to 100 nucleotide bases in length.

10 13. The nucleic acid sequence of claim 11, wherein said nucleic acid sequence sequence is 15 to 25 nucleotide bases in length.

14. The nucleic acid sequence of claim 11, wherein said at least one variance comprises a variance listed in Table 3.

15 15. A method for determining the presence or absence of a variance in a gene selected from the group consisting of Human glutamate dehydrogenase (EC 1.4.1.3., GDH), Cytochrome P-450 (CYP3A4), Human acyl coenzyme A:cholesterol acyltransferase, Homo sapiens P-type ATPase FIC1, Human neutral amino acid transporter B, Human E16, H.sapiens canalicular multidrug resistance protein, Human organic anion transporting polypeptide (OATP), Carboxylesterase I, H.sapiens REC1L or a sequence complementary thereto or an RNA equivalent comprising contacting at least a portion of said gene or a sequence complementary thereto with a probe as described in claim 1 under selective binding conditions.

20 25 16. The method of claim 15, wherein said at least one variance comprises a variance listed in Table 3.

add
a 1

ADD
8'